



## Autism Spectrum Disorder Prediction Using Machine Learning and Design Science

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DOI:<https://doi.org/10.52756/ijerr.2024.v39spl.017>

**Abstract:** Machine learning, a subset of Artificial Intelligence, has gained much recognition in facilitating disease prediction and the decision-making process in healthcare. One of the most often diagnosed developmental disorders in the world is Autism Spectrum Disorder (ASD). Around the world, it is reported to afflict 75 million people and the number of cases has gradually increased since studies began in the 1960s. The symptoms generally include communication deficits, sensory processing differences, and repetitive actions or behaviors. This research develops a model to detect ASD using Principal Component Analysis and Machine Learning algorithms to classify and predict the risk of ASD among pregnant women. Data was collected from National Hospital in Abuja, Nigeria. According to the results, PCA and Random Forest produced the best accuracy of 98.7%. Bayesian probability was employed to evaluate and verify the reliability of the model. The created model can aid doctors in diagnosing ASD.

## Introduction

Autism spectrum disorder (ASD), a neuro-disorder disease has a long-term impact on an individual's capacity to engage and interact with others. Since symptoms of autism typically show in the initial phase of a child's life, it is considered a "behavioral disease" and can be diagnosed at any point in life (Raj et al., 2020). One of the most often diagnosed developmental disorders today is ASD. Around the world, it is reported to afflict 75 million people, and the number of cases has gradually increased since studies began in the 1960s. The symptoms generally include communication deficits, sensory processing differences, and repetitive actions or behaviors. It also exists as a spectrum divided into 3 levels, each based on the severity of these symptoms

(Hugues et al., 2021). Scientists are focusing on strategies to identify ASD as early as possible, as early intervention of therapy is crucial for children with autism. Today, a reliable diagnosis can be made as early as the child is 2.

No simple diagnostic tool is available, such as X-rays for fractured bones or blood testing for diabetes. It is more difficult to diagnose autism because it can only be done based on behavior. Parents and doctors frequently miss out on children with less severe symptoms; more severe cases may look like other developmental abnormalities (Amin et al., 2023). Researchers at the University of Limoges in France recently created a computer program that uses fetal traits to predict whether a child will be diagnosed with autism as early as one day after birth. Early detection of autism would enable



families to start the communicative, social, and sensory therapy that may be essential to the development of the autistic child (Hugues et al., 2021).

Technology has been used in the health sector for purposes like monitoring, evaluation, awareness etc. Machine learning, a subset of artificial intelligence, is the most effective tool for achieving these goals, whether the objective is to predict reality or find hidden patterns, using patterns to uncover some hidden patterns of future data (Srivastava and Tripathi, 2023; Singh and Sharma, 2023; Singh et al., 2023). ML methods are very effective in disease recognition (Haloi et al., 2023; Gajbhiye et al., 2023). These diseases may be related to plants (Kumar et al., 2021; Rukhsar et al., 2022; Upadhyay et al., 2021; Upadhyay et al., 2022) or animals. However, as a machine learning model's efficiency frequently depends on the training data and corresponds to the computer term "garbage in, garbage out," the method used to collect data frequently affects the model's performance (Zhang et al., 2021). Inconsistent data, defined as incorrect data entry, is the most common issue in data collection. To thrive in this discipline, feature engineering and selection techniques are used to manipulate data when developing models. Feature selection is "reducing the height of the data by finding a set of features that describe the data well" (Khaire et al., 2019). Considering the observations, feature selection is critical to ensuring that only crucial features are utilized in the design to reduce the number of disparities between data and optimization for well-defined prediction models.

Autism is a systemic disorder that affects the brain and is not a genetic brain disorder. Certain genes are activated in people predisposed to this disorder by a hazardous environment. ASD is a neurological condition that causes children to have a lifelong dysfunction that leads to mental disease (Kundu, 2019). As a result, precautions should be taken to diagnose the illness as early as possible (Marin et al., 2019). In the field of clinical and scientific research, autism is still exceedingly challenging to diagnose during pregnancy or right after birth. Compared to statistical analysis, using machine learning classifiers has been proven to increase the accuracy of health prediction (Sivaram, 2022). Stress has emerged to be an integral part of every person's life in today's competitive and rival world, affecting an individual directly or indirectly in many traditions (Mittal et al., 2022). The results of predictive classification algorithms need to be verified using real-world information. Overcoming the problem of interpretability among health practitioners is one concern. When interpretability is good, it is simpler for healthcare

professionals who must use it to trust the conclusions made by such models. This study aims to fill in these knowledge gaps by building a model to predict autism spectrum disorder utilizing PCA and machine learning classification analysis.

Design Science (DS) research aims to generate prescriptive knowledge about the design of artifacts, such as software, methods, models or concepts. It includes six steps: problem identification and motivation, objectives, design and development, demonstration, evaluation, and communication. This paper explored the concept of DS and the impact of feature engineering algorithms such as scikit-learn random samplers to generate synthetic data for predictive models where data is weak or inconsistent due to many outliers. In addition, a comparative analysis of the literature has been done to identify the most effective model for predicting ASD (Viloria et al., 2020). The models identified in literature with high performance will be used on the dataset, using the same model evaluation metrics in the literature to draw a valid conclusion.

The aim of this study is to build a machine-learning prediction model for autism spectrum disorders. Following are the objectives of this study:

- i. Carry out an Exploratory Data Analysis (EDA) on the dataset.
- ii. Build a model for prediction using PCA and machine learning classification algorithms for ASD on baseline data.
- iii. Validate the model to improve performance accuracy using a k-fold cross-validation technique.
- iv. Employ Bayesian probability to assess the model's reliability.
- v. Compare the best-performing model with a similar existing model in the literature.

This paper is summarized as follows: Section 2 presents a literature review, Section 3 presents the methodology used in the research, Section 4 presents experimental results and finally, Section 5 concludes the work.

## Literature Review

This section looks at the various definitions of key concepts and works that show how other researchers have predicted autism spectrum disorder using machine learning techniques.

## Autism Spectrum Disorder (ASD)

A neuro-disorder known as ASD has a long-term impact on an individual's capacity to engage and interact with others. Autism is a "behavioral disease" as symptoms typically develop in the initial phase of a child's life, but it can be diagnosed at any point in one's

life. ASD claims that the issue begins in childhood and persists into adolescence and adulthood (Raj et al., 2020). They examined retrospective ultrasound and biological measurements of infants diagnosed later with ASD or neuro typical (NT) that are regularly gathered during pregnancy and birth to identify infants at risk of developing ASD and to detect ASD biomarkers early after birth (Caly et al., 2021). An automated ASD prediction model was created by (Vakadkar et al., 2021) using minimal behavioural sets taken from each diagnosis dataset. By using the Q-CHAT-10 dataset, the developed model predicts autism spectrum disorder with 93.84%, 81.52%, 94.79%, 97.15%, and 90.52% accuracy in the case of Support Vector Machines, Random Forest Classifier, Naïve Bayes, Logistic Regression, and K Nearest Neighbour, respectively. Comparing all five supervised machine learning algorithms, Logistic Regression and Naïve Bayes algorithms had the best accuracy in the detection of autism spectrum disorder.

ASD is a disorder that affects one in a hundred kids worldwide. ASD considered the effects of socioeconomic, ethical, and regional characteristics on prevalence estimates. Estimates of prevalence changed over time and were very variable both within and between socio demographic groupings. Researchers have made significant progress in the development of health information systems, especially standardized clinical coding systems (Mahdi et al., 2023). For guiding public policy, increasing awareness, and establishing research goals, prevalence estimates of autism are crucial. These results reflect modifications to the criteria of autism as well as variations in the methods and environments used in prevalence studies (Zeidan et al., 2022). Patients with autism deal with a variety of difficulties, including attention problems, learning disabilities, mental health issues including anxiety, depression, etc., motor difficulties, sensory issues, and many others. Autism is currently on the rise in large numbers and at a rapid rate throughout the world. The World Health Organization (WHO, 2017) estimates that one in 160 infants suffers from ASD. While some people with the disorder can live independently, others need care and support for the rest of their lives. Autism diagnosis takes a long time and costs a lot of money. Early diagnosis of autism is very crucial in terms of providing patients with the right medicine at the right time. It could stop the patient's illness from getting critical and could lower long-term expenses bring on by a delayed diagnosis (Omar et al., 2019).

## Machine Learning

Machine Learning classifiers have proved to improve health prediction accuracy over statistical analysis (Sivaram, 2022; Upadhyay et al., 2024). One of the foundation features of machine learning is to learn to train themselves for different circumstances, reducing the need for manual human involvement as much as possible. In modeling development, there are the phases of testing and training. Learning occurs during training by giving it a dataset and an algorithm. ML methods automatically identify important predictive features and predict risks from early pregnancy (Liu et al., 2022). Currently, electronic health records (EHRs) offer detailed evidence about demography, patient's medical history, medications, laboratory test results, and doctor's diagnosis (Odu et al., 2022), which serves as a dataset in most healthcare research. A dataset is a collection of complete, usually massive, data used to train the system. Datasets are an important part of every machine learning system, and using ML techniques may help enhance the prediction model (Shtar et al., 2022). It must be broad and large enough to allow the system to learn to work under various conditions. Another key aspect is the algorithm, which outlines how the system is expected to understand the presented dataset. Popular, basic algorithms like Regression, Random Forests, Decision Trees, and so on are utilized in various applications. The now-trained system is tested using various data records during the testing phase, and the accuracy of the predictions is utilized for training the system further, making it a continuous and typically iterative process (Jabi et al., 2021).

Artificial Intelligence (AI) has focused on developing machines capable of performing human tasks. In order to achieve human performance capabilities, these machines can learn and extract insights from the data (Ronmi et al., 2023). The research of methods computer systems use to complete categorization tasks without the need for external instructions, mostly utilizing learned models, is known as machine learning (Sufriyana et al., 2020). Supervised learning and unsupervised learning are the two main categories into which classification techniques for intrusion detection may be separated. The supervised approach uses the characteristics of the already available data as input to produce desired results, and the algorithm generates an inferred function known as a classifier or regression function. This approach provides quick calculation, minimal false alarm rates, and great accuracy. Unsupervised learning is a technique that produces results based on the properties of the current data input (Villalaín et al., 2022). Boolean logic is a

superset that has been expanded to include fuzzy logic, which can handle the idea of partial truth-to-truth.

### Random Forest

In Random Forest, the planned strategy is to divide and conquer. It generates many Decision Trees that are all learned by selecting any subset of traits from the entire collection of predictor attribute values. Each tree is limited in how much it can grow by the property in the subset. The final Decision Tree will then be constructed for the projection of the test dataset using the average or weighted average method. A random forest differential measure can be used to quantify unstructured data. The data shown are the unaltered, original data collected from a variety of references. Since it can successfully handle mixed variable types and is invariant to repeated input variable changes, dissimilarity calculated using a random forest is favorable (Schonlau et al., 2020).

### Decision Tree

The decision tree algorithm is within the domain of supervised learning algorithms. The decision tree approach can be utilized to fully understand the classification and regression problems, in contrast to conventional supervised learning algorithms (Franchuk et al., 2021).

### Naïve Bayes Algorithm

A supervised learning technique and a statistical classification technique are both demonstrated by the Naive Bayesian Classification. By calculating the probabilities of the results, the naive Bayes algorithm establishes an underlying probabilistic model and enables thoughtfully capturing ambiguity about the model. It may also be applied to answer diagnostic and predictive questions (Ghandi., 2018).

### Research Gap and Our Contribution

Out of the examined articles, found a gap in the work of Vakadkar et al. (2021) who developed a prediction model to detect autism behavioral traits. By using the Q-CHAT-10 dataset, the developed model predicts autism spectrum disorder with 93.84%, 81.52%, 94.79%, 97.15%, and 90.52% accuracy in the case of Support Vector Machines, Random Forest Classifier, Naïve Bayes, Logistic Regression, and K Nearest Neighbour, respectively, for better detection of autism spectrum disorder. Comparing all five supervised machine learning algorithms, LR and NB algorithms are practical for better detection of autism spectrum disorder.

This study uses principal component analysis (PCA) for feature selection and a k-fold cross-validation technique to optimize the result (Vakadkaret al., 2021). The accuracy of the model was 98.7%. The Bayes theorem was also used to test the reliability of the findings and the model is evaluated using the Confusion Matrix. Furthermore, the performance accuracy for the real dataset gave better and more reliable results.

### Method And Materials

This chapter presents the methodology adopted for this research. The subheadings below were followed as the process was taken to develop the model and achieve the objectives of the study.

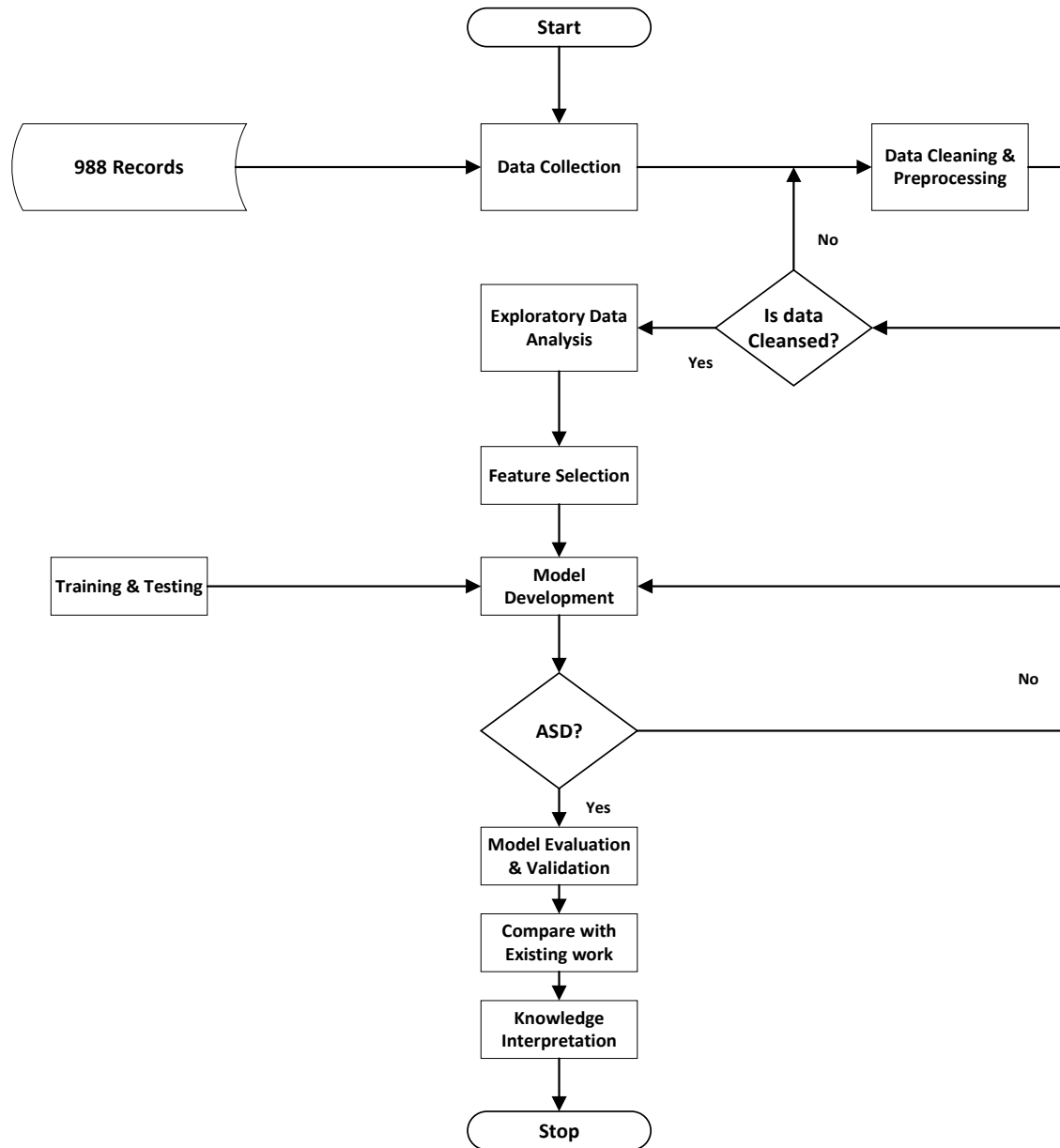
### Research Method

The study employed a design science approach along with a quantitative experimental design. Abuja, the capital of Nigeria, is the only geographical area used. The aim of this research is to detect ASD in pregnancy among pregnant women at the National Hospital, Abuja. Figure 1 show the proposed framework (PPRF), which illustrates the method used to accomplish the objective of this research. Data collection, exploratory data analysis, and preprocessing which comprise data cleansing and handling missing values, come first in the study. And then, Principal Component Analysis (PCA) was used for feature selection and k-fold for evaluation and validation. Following that, the three algorithms—Decision Tree, Random Forest, and Naive Bayes, are used throughout the model development phase. The characteristics of the models were taken into consideration when conducting the analysis. Results from the three classification models were contrasted. The classification models were evaluated using the confusion matrix, Receiver operating characteristic Curve (ROC), and Area under Curve (AUC). The best accuracy (98.7%) was achieved by using Random Forest algorithm. The model's reliability was assessed using Bayes Theorem. In the last stage of the experiment, the result is compared to findings from similar existing models. Python programming language was used to implement the models.

### Dataset and Data Collection

The National Hospital Abuja, repository served as the source for the dataset. An interview between (the patients and the doctor) served as the data collection method. There are 998 samples.





**Figure 1. Proposed Framework (PPRF).**

**Table 1. Contents of Dataset.**

Attributes	Values	Numbers
Class	YES	499
	NO	499
Preterm Birth	YES	692
	NO	306
Primipara	YES	377
	NO	621
Family History	YES	254
	NO	744
Personal History	YES	274
	NO	724
Gestational diabetes	YES	655
	NO	343

Preeclampsia	YES	691
	NO	307
Deficiency in vit D	YES	363
	NO	635
Age	Integer Values	(in ranges)
BMI	Integer Values	(in ranges)

**Table 2. First 11 rows of the Autism Dataset.**

Sn	Age	Preterm birth	Gestational diabetes	preeclampsia	Family-History	Personal-History	Deficiency in Vit D	Primipara	BMI	Class
1	34	YES	YES	YES	NO	NO	YES	YES	92	YES
2	30	YES	YES	YES	NO	YES	YES	NO	108	YES
3	41	YES	YES	YES	NO	NO	YES	NO	110	NO
4	21	YES	NO	NO	NO	NO	YES	NO	86	YES
5	24	YES	YES	YES	YES	NO	YES	NO	99	YES
6	36	YES	YES	YES	NO	NO	NO	YES	102	NO
7	27	YES	YES	YES	NO	NO	YES	NO	95	YES
8	25	YES	YES	YES	NO	NO	YES	YES	89	YES
9	39	YES	YES	YES	NO	NO	YES	YES	94	YES
10	38	YES	YES	YES	NO	YES	YES	NO	135	NO
11	37	YES	YES	YES	NO	NO	YES	YES	112	YES

**Table 3. Attributes and Values of the Dataset.**

Attributes	Category	Values
Class	YES	499
	NO	499
Preterm Birth	YES	692
	NO	306
Primipara	YES	377
	NO	621
Family History	YES	254
	NO	744
Personal History	YES	274
	NO	724
Gestational diabetes	YES	655
	NO	343
Preeclampsia	YES	691
	NO	307
Deficiency in vit D	YES	363
	NO	635

Table 1 displays the numbers and values of the dataset. This dataset has ten (10) attributes. The class column distinguishes the problem (Autism YES, Non-Autism, NO). Based on domain knowledge, there are nine (9) independent variables (Preterm Birth, Primipara, Family History, Personal History, Gestational diabetes, Preeclampsia, Deficiency in vit D, Age, BMI (KG), and one (1) dependent variable (Class).

Table 2 displays the summary of the dataset's first 11 records along with an overview of the data. Nine of the ten columns are attributes. The last column is the class column.

Table 3 shows the class variable, which includes 499 Yes to indicate that 499 people have autism and 499 No to indicate that 499 people don't, displays the category attributes and their values.

### Pre-processing

In the pre-processing stage, values or feature changes that could have a negative effect on the model are carefully cleaned up and eliminated. Pre-processing data sought to change it into a format that could be used for model fitting and further analysis. During the pre-processing stage, pre-bias in the data were removed, and randomization techniques and Imputation of missing values were used. The technique employed in this research to prepare the data includes data integration, dimension reduction, data standardization, and management of missing and noisy data. Noisy data were smoothed before being used to forecast data that hasn't yet been observed, and outliers were found and eliminated from the dataset. The idea of exploratory data analysis was developed to explore, visualize, analyze, process, and interpret data variations and relations.

A correlation plot was utilized to show how the features were correlated. The model used the column feature set as a vector of values, and these feature values or vectors were connected. Utilize the covariance coefficient of the feature vectors, which is obtained by taking the dot product of the two feature vectors, for this. The sign denotes the direction in which variation and the feature change with other features, either increasing or decreasing. Equation (1) provides the formula:

$$\text{Cov}(x,y) = \text{Sum}((x - \text{mean}(x))(y - \text{mean}(y))) / n \quad (\text{Musa et al., 2024}) \quad (1)$$

where  $x$  and  $y$  are the two features.

Use correlation, which is the cosine angle between the two vectors, rather than covariance. Correlation values range from -1 to +1. It only provides the variation's

direction. 'std' stands for Standard Deviation in the formula. The formula is given by Equation (2):

$$\text{Correlation} = \text{corr}(x,y) = \text{Cov}(x,y) / \text{std}(x).\text{std}(y) \quad (\text{Musa et al., 2024}) \quad (2)$$

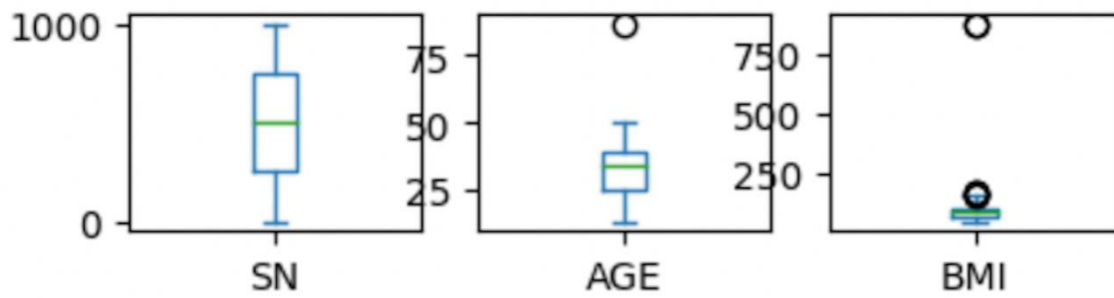
Scale and dimension are not correlation factors. It is crucial to understand the correlations between the features to employ only one of the features with a very high correlation. After all, frequently refer to the same piece of knowledge. Additionally, you should only utilize features that have a weak association with the target values because they have minimal impact on a prediction but add to the model's complexity. The plot's outcome displays the size and the hues, which signify how the two features are related to one another. The closer the variable value is to 1, the stronger the correlation. To this end, Preterm birth and Preeclampsia have a high correlation, followed by Gestational diabetes and body mass index (BMI) with a low correlation. Additionally, it indicated that complex modeling methods might not be necessary. The Python programs and libraries Seaborn and Matplotlib were used to create a correlation plot for this investigation.

### Exploratory Data Analysis

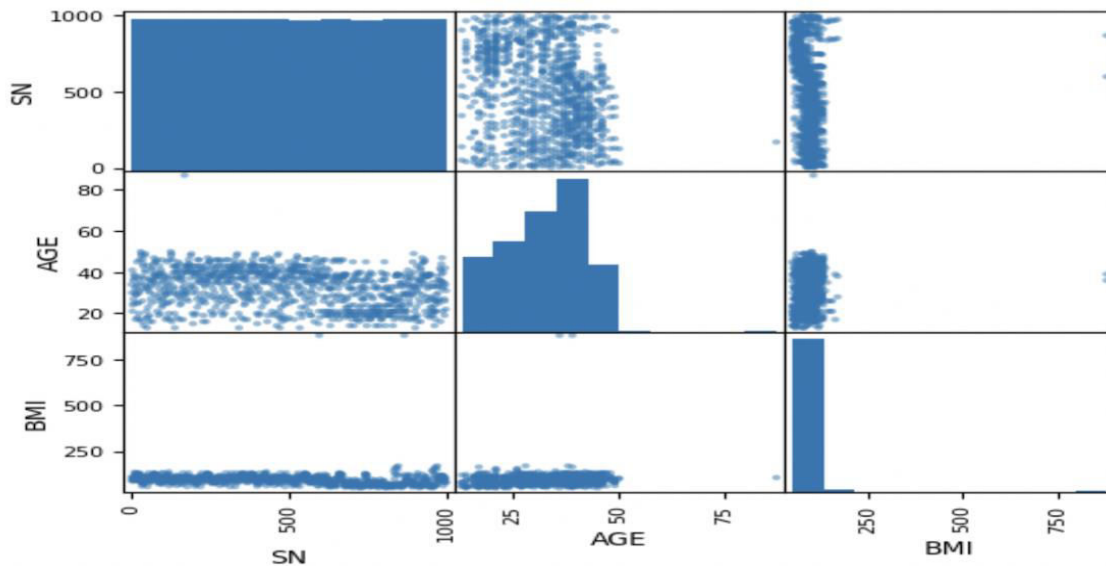
The idea of exploratory data analysis was developed to explore, visualize, analyze, process, and interpret data variations and relations. At this point, anomalies were found. Exploratory data analysis aids in displaying potential predictive models for the dataset presented. Histograms are frequently plotted for categorical variables, category counts, and numerical variables reflecting the distribution.

When category (binary) dependent variables were employed to compare various numeric variables, the box and whisker plots of the few density plots overlapped. The variable density charts discriminated between ASD and NON-ASD. In Figure 2 below, the box plots make the outliers easier to see. The solid box primarily lies between the first and third quartiles. The isolated points are the outliers, while the bars represent the distributions' greatest and lowest points of numerous occurrences. They must be eliminated since they make the model less accurate. The two boxes display the continuous data's fluctuation with respect to the categories.

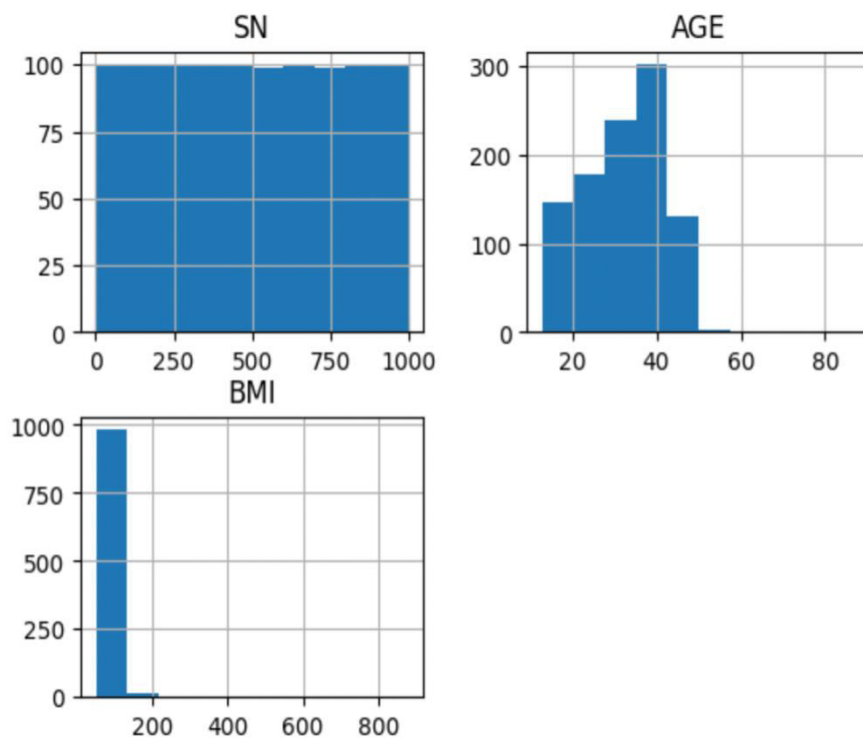
Box plots are a graphical representation of the numerical data through their quartiles. The lower and upper whiskers are like boundaries of the data distribution.



**Figure 2. Box and Whisker Plot of the dataset.**

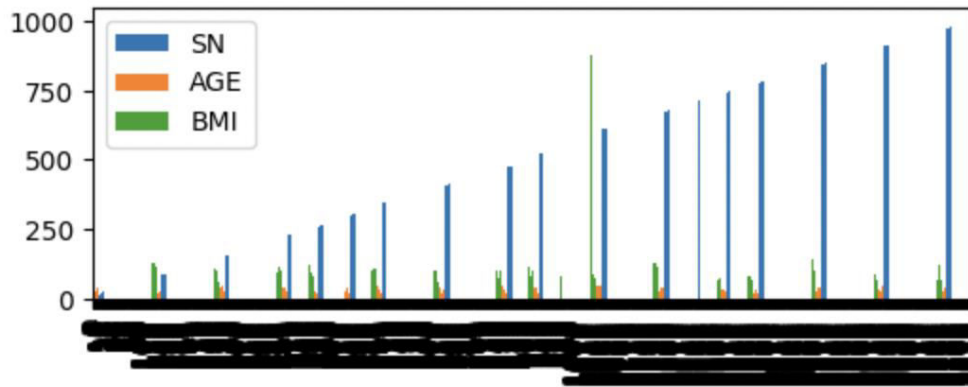


**Figure 3a. Distribution and Statistical Summary of the Dataset.**



**Figure 3b. Distribution and Statistical Summary of the Dataset.**





**Figure 3c. Distribution and Statistical Summary of the Dataset.**

Minor overlap is shown in the graphical distribution of the attributes in Figures 3a, 3b, and 3c, but there are different distributions for each class of values for each of the attributes. This is a promising indication that the qualities and classes can be distinguished. Despite this, only a small number of attributes may have a Gaussian-like distribution in any way. This demonstrates that the distribution may likely become Gaussian when more data are collected. A skew or a significant number of occurrences towards the top right end of the distribution may be present for some characteristics, such as BMI. Also, the attribute age does not increase or is irrelevant to the model's predictive value. The figures within the lines show each group's absolute frequencies throughout the entire data collection. Several inferences can be made from the graph.

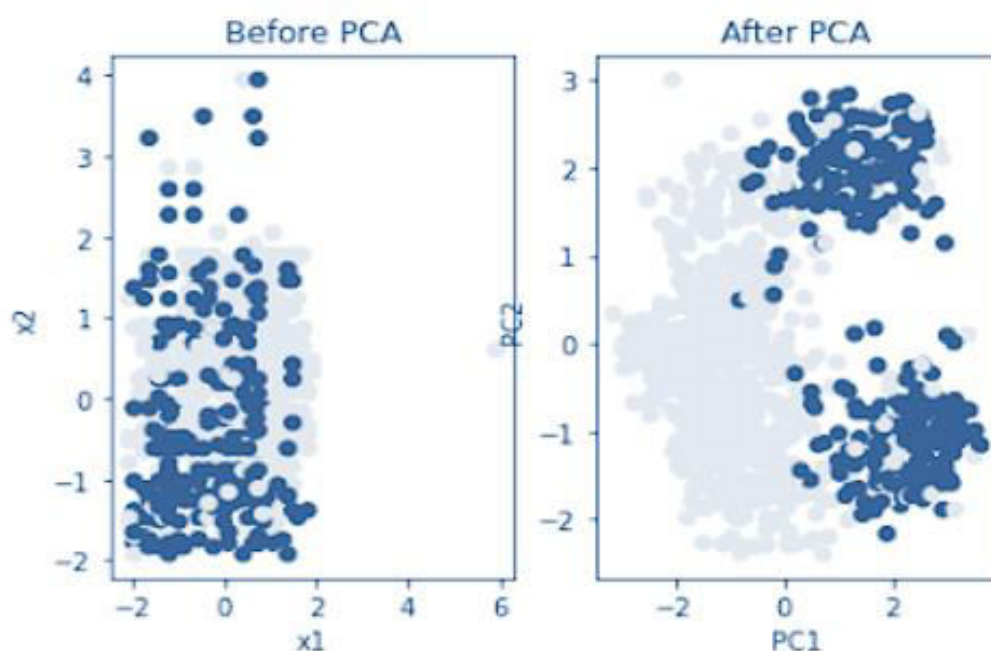
#### Feature Selection using Principal Component Analysis (PCA)

Feature reduction is the process of reducing the input

parameter to a model by using only trivial data and eliminating noise. Data preparation for modeling was done. A significant part of the data preparation involved transforming the dataset to include rescaled attribute values and attributes broken down into components. The process of feature selection was also employed to prepare the data. To deal with redundant features in the data that can reduce the models' accuracy, feature selection was carried out.

A set of information used to train predictive models significantly impacts how well they function; as a result, feature selection speeds up the training process while addressing issues like overfitting and misleading data. The attributes in the data that are most important for prediction were chosen using principal component analysis, or PCA.

Machine learning typically relies on differences in how Data Points behave across various classes. Low variance implies that points will tend to cluster around



**Figure 4. Feature Importance from PCA Analysis.**

one another, making it difficult to distinguish between them.

In Figure 4, the result of PCA and important features are shown. Preterm birth, Preeclampsia, Gestational diabetes, and BMI are correlated with ASD and have a higher importance in the matrix. ASD data has some characteristics. Depending on the feature, these ranges can vary between 0 and 1; while others have values between 10 and 100. The scale utilized in the study, which has values ranging from 0 to 1, is known as Min-Max Scaling. The variation was greatest in the PCA space along PC1, which accounts for 23% of the variance, and PC2, which accounts for 15% of the variance. Together, they account for 38%. The maximum variance proof can also be seen by calculating the covariance matrix of the smaller space.

### Algorithm Training and Model Development

The study used three machine learning classifiers: Decision tree, Random Forest, and Naive Bayes. Employed k-fold cross-validation, each fold's sample is randomly selected without replacement. Specifically, two approaches were considered.

- i. Model evaluation of the baseline data (original data)
- ii. Model evaluation of the data with feature importance

The best-performing model on the validation set was tested on the test set to evaluate how well it would typically hold. To increase accuracy, the model's training was done again with new input parameters for the selected attributes. The model performance was enhanced using a k-fold, which is more reliable.

### Evaluation of Model Performance

The confusion matrix, ROC-AUC, and Bayesian test are the parameters used to assess and test the model's performance and reliability.

#### Confusion Matrix

The number of correct and incorrect predictions made by the classification model in relation to the actual results of the data (the goal value) is displayed in the confusion matrix. N is the number of target values (classes), and the matrix is N×N. It is common practice to evaluate the efficacy of such models using the information in the matrix. The effectiveness of the model was assessed using a confusion matrix. The confusion matrix was used to determine whether the model with binary goal values was applicable (0 or 1). Each value of the confusion matrix was established using the results of the model testing.

True positives (TP): Number of correctly classified tuples from the positive class.

False negatives (FN): Number of incorrectly classified tuples from the positive class.

False positives (FP): Number of incorrectly classified tuples from the negative class.

True negatives (TN): Number of correctly classified tuples from the negative class.

Accuracy: Proportion of correctly classified tuples (Musa et al., 2024).

$$TPR = \frac{\text{No. of correctly predicted PE}}{\text{Total number of PE}} \times 100$$

$$TNR = \frac{\text{No. of correctly predicted nonPE}}{\text{Total number of non PE}} \times 100$$

The formula is given by Equation (3):

$$FNR = \frac{FN}{TP + FN} \quad (3)$$

The false Positive Rate accounts for the percentage of the negative class incorrectly classified by the classifier. The formula is given by Equation (4):

$$FPR = \frac{FP}{TN + FP}$$

$$FPR = 1 - \text{Specificity} \quad (4)$$

**F-Score:** In this work employed the F1-score as the main measure for assessing models, which is described as the harmonic mean between the two (Han et al., 2012). The F1 score depends on whether the class is classified as positive according to how accuracy and recall are defined. High accuracy is important for prognosis since false positives are expensive (Musa et al., 2024).

F1 Score: it's the combination of sensitivity and recall. It's represented by  $(2 * \text{Precision} * \text{Recall}) / (\text{Precision} + \text{Recall})$  (Musa et al., 2024). The formula is given by Equation (5):

$$F\text{-score} = 2 * ((\text{precision} * \text{recall}) / (\text{precision} + \text{recall})) \quad (5)$$

**Precision:** is the division of the positive cases correctly identified by all the cases identified as positive (including false positives) (Musa et al., 2024). The formula is given by Equation (6):

$$\text{Precision} = TP / (TP + FP) \quad (\text{Hossain et al., 2021}) \quad (6)$$

**Recall:** Recall and true positive rate (TPR) is the proportion of positive tuples that were correctly classified. However, recall is also crucial since finding a decent amount of possible risk is what the problem is all about. The formula is given by Equation (7):

$$\text{Recall} = TP / (TP + FN) \quad (\text{Hossain et al., 2021}) \quad (7)$$

**False positive rate (FPR).** FPR is the proportion of incorrectly classified negative tuples False Positive Rate (FPR) =  $FP / (FP + TN)$  (Musa et al., 2024)

**Accuracy:** represents the number of correct predictions divided by the total number of predictions. In

categorization tasks, accuracy is the percentage of correct predictions the model makes over all other predictions. Accuracy is a useful metric in the highly equilibrated target variable classes of data (Musa et al., 2024). The formula is given by Equation (8):

$$\text{Accuracy} = (\text{TP} + \text{TN}) / (\text{TP} + \text{FN} + \text{FP} + \text{TN}) \quad (8)$$

**Specificity:** the same as recall, but for negative examples: it's the division of the true negatives by all the real negative cases (including false positives) (Musa et al., 2024). The formula is given by Equation (9):

$$\text{Specificity} = \text{TN} / (\text{TN} + \text{FP}) \quad (9)$$

**Sensitivity:** is the division of the true positives by all the real positive cases (including false-negative cases). When striving to have more true positives than true negatives, it counts. The model's sensitivity measures its capacity to detect preeclampsia. The percentage of positive cases predicted to be positively served as the sensitivity measure. Sensitivity describes the percentage of the positive class correctly classified and inferred from the confusion matrix (Musa et al., 2024). The formula is given by Equation (10) below:

$$\text{Sensitivity} = \text{TP} / (\text{TP} + \text{FN}) \quad (10)$$

$$\text{Error rate} = 1 - \text{Accuracy} \quad (11)$$

### Receiver Operating Characteristic (ROC) and Area under the Curve (AUC)

The Receiver Operator Characteristic (ROC) is a curve for experimental binary class problem metrics. It is used to visualize the performance of a binary classifier and it shows the trade-off between the true positive rate and the false-positive rate. A ROC area of 1 represents a perfect test and 5 represents a worthless test. It is an excellent method for measuring the performance of a Classification model. The True Positive Rate (TPR) is plotted against the False Positive Rate (FPR) for the probabilities of the classifier predictions (Musa et al., 2024). Then, the area under the plot is calculated.

The curve shows the trade-off between the true and false-positive rates.

True Positive Rate = True Positive / (True Positive + False Negative)

False Positive Rate = False Positive / (True negative + False Positive)(Musa et al., 2024).

The Area under the Curve (AUC) was interpreted as a criterion of the capacity of a classifier to differentiate between different classes of the plots and is also used as an overview of the ROC curve. A strong model has an AUC close to 1, indicating that it has a high level of distinction. An AUC close to 0, which indicates the poorest measure of separability, indicates a bad model. It indicates that the outcome is being reversed. It predicts both 1s and 0s as 1. Additionally, when AUC =1, it means that the classifier can perfectly distinguish between all the positive and negative class points.

### Bayesian Test

To reassess the model's performance with known sensitivity, the study ran a Bayesian test on the model of choice. The concept of the Bayesian theorem was implemented. The formula for Bayes' theorem is given in Equation (12) below:

$$P(B) = \frac{P(A)P(A)}{P(B)} \quad (\text{Musa et al., 2024}). \quad (12)$$

### Comparison of Findings with Existing Model

The benchmark study (Vakadkar et al., 2021), which was used as a comparison, had an accuracy of 97.15%, and the Q-CHAT-10 dataset (1054 datasets) and 18 attributes were collected from people with autistic and without autistic symptoms were used to evaluate the study model.

### Analysis

The data was analyzed to cover the stages of the machine learning model design, and the results were used to achieve the study objective of predicting autism spectrum disorder using the PCA and ML algorithms.

### Model Results

Table 4 demonstrates the results of the three algorithms used in the study and, using the ROC curve

**Table 4. Result of Classifiers.**

Models	Time taken (s)	Accuracy (%)	Precision	F Score	Sensitivity	Specificity	ROC/AUC
<b>Proposed Model (PPRF)</b>	0.0312	98.7	0.96	0.93	0.97	0.79	0.96
<b>Decision tree</b>	0.0562	95.6	0.94	0.91	0.92	0.75	0.71
<b>Naive Bayes</b>	0.0725	97.2	0.96	0.89	0.91	0.67	0.69

and confusion metrics parameters evaluates the classification model's visual performance. Three algorithms were used in the analysis. The characteristics of the models were taken into consideration when conducting the research. The visual of how well the categorization model performs is evaluated using the ROC curve. In the given situation, choose a threshold level using the curve that strikes a balance between sensitivity and specificity. A flawless classifier will have a ROC AUC of 1, while an entirely random classifier will have a value of 0.5.

The result (Table 4) showed that random forest has the best accuracy at 98.7% with a standard deviation of .084. The model took 0.0312seconds to perform or run. The precision score was 0.96, the recall (sensitivity) was 0.97, and the F-score was 0.93. The specificity was 0.79, and ROC was 0.96. Showing the reliability of the classifiers to predict or tell the nature of diseases (ASD).

The result for the Decision Tree showed an accuracy of 95.6% with a standard deviation of .079. The model took 0.0562 seconds to perform or run. The precision score was 0.94, the recall (sensitivity) was 0.92, and the F score was 0.91. The specificity was 0.79, and ROC was 0.71.

The result from Naive Bayes showed that the accuracy was 97.2% with a standard deviation of .082. The model took 0.0725 seconds to perform or run. The precision score was 0.96, the recall (sensitivity) was 0.91, and the F score was 0.89. The specificity was 0.67, and ROC was 0.69.

From Table 5, accuracy of 98.7% proves that it is relatively more successful in predicting ASD; this was also supported by the domain knowledge and the possibility that the disease is relatively common in the general population of the sample data. The F-score is lower than accuracy measures as it embeds precision and recalls into its computation.

### Reliability Testing (Bayes Theorem)

The strong classifier can be given additional influence, which considerably improves classification performance, by using the Bayesian formula to dynamically update the weight value for each tree (Zhang et al., 2021). By considering the incidence rate and applying the Bayes theorem, we can assess how effectively the machine learning classifier works and determine whether the result is reliable enough to be used in a typical clinical scenario. Analyze the specificity and sensitivity of the result to determine its validity using the Bayes theorem. That is how frequently true positives and true negatives are found by the test. This makes it easier to assess the value of binary classifiers.

Event A = unconditional probability of this disease in the population (population = 998; those with diseases = 50%, those without disease = 50%, specificity/sensitivity = 97%, 1- specificity = 0.03)

$P(A)$  = presence of the disease

$P(A) = 0.50$ .

Event B= unconditional probability of our test coming up positive.

**Table 5. Proposed Model and Similar Existing Model on Autism Spectrum Disorder (ASD) Prediction.**

Parameters/ Evaluation model	Proposed model (PPRF)	After comparison with a similar existing model (Vakadkar et al., 2021)	Similar Existing model (Vakadkar et al., 2021)
<b>Parameters</b>	Accuracy = 98.7% Time taken = 0.0312s Specificity = 0.79 Precision = 0.96 Population = 998 F score = 0.93	Accuracy = 97.7% Time taken = 0.0553s specificity = 0.71 precision = 0.97 Population = 998 F score = 0.91	Accuracy = 97.15% Specificity = 0.68 Precision = 0.90 Population = 1054 F - score = 0.89

### Comparison with Similar Existing Work

The findings of this study, as shown in Table 5, compared the result of Random Forest ASD prediction with (Vakadkar et al., 2021), which had an accuracy of 97.15%. The algorithm of (Vakadkar et al., 2021) is being implemented under the same environment by reducing the data set to 998 samples, which got an accuracy of 97.7%.

$P(Bt)$  (True Positives) =  $998 * .50 * 0.97 = 484.03$

$P(Bf)$  (False Positives) =  $998 * .50 * 0.03 = 14.97$

$P(B)$  (total positives) =  $(484.03 + 14.97) / 998 = 0.5 = 50.0\%$

$P(B|A)$  = probability of getting a positive result regardless of whether it's a true-positive or not,

Thus  $P(B|A)$  = sensitivity.

$P(B|A) = 0.97$ .

$P(A|B) = 0.97 * 0.5 / 0.5 = 97\%$



In all the calculations, Random Forest in the study performed better than the other models because of its ability to use different feature subsets and decide at different classification stages. The outcomes demonstrated that the model's ROC AUC was approaching 1. Thus, the classifier is likely effective at determining if a pregnant woman is carrying a child that will likely be born with ASD.

The drawback of the model is that the total sample used for training the model was small when compared to the work of (Vakadkar et al., 2021). However, the study extends the scope of literature by subjecting results to the Bayes theorem to evaluate its overall reliability.

## Conclusion

This section presents summary, contribution to the body of knowledge, conclusion and recommendation.

## Summary and Discussion

The study developed an autism spectrum disorder prediction model using machine learning tools and algorithms. Predicting the disorder in pregnancy among pregnant women was possible using PCA, and machine learning tools. The machine learning model of focus was the random forest, decision tree, and naïve Bayes. The findings showed that PCA and Random Forest could predict the occurrence of ASD, and results from the Random Forest showed that the accuracy was 98.7%, with a standard deviation of .084.

## Contribution to the Body of Knowledge

To forecast ASD, the study developed a supervised model. This model was improved using the unsupervised learning clustering technique, which selected the best feature and optimized the threshold while predicting a class. The most significant features of the patients that cause the diseases were uncovered in the research. The strongest correlated aspects of the diseases were visualized using machine learning algorithms because interpretability is a challenge for non-computer data scientist professionals. The study advances knowledge of how critical it is for physicians to use machine learning and feature-importance algorithms to detect ASD in pregnant women at risk before birth. Although models cannot capture the clinical impacts caused by bias or incorrect calibration, the investigation's usage of a Random Forest yielded encouraging results. It was discovered that the Bayes theorem validates the model's reliability. This method considerably boosted the advantages for patients and provides a threshold probability-based evaluation viewpoint on predicting ASD. This work contributes to the body of knowledge

regarding the use of PCA and machine learning algorithms in the prediction of ASD.

## Conclusion and Recommendations

In this study, classification, clustering, and machine learning techniques were proposed for the prediction of ASD in pregnant women. The results revealed that characteristics that can predict ASD among pregnant women at risk of having babies with ASD were analyzed using PCA and Machine learning methods in this research. The resulting Machine learning model is utilized by doctors as a useful prediction tool to early detect people who are pregnant with the condition. Another conclusion from this research is Primipara, Age, and Personal History do not improve the prediction efficacy of the ASD model.

It is recommended that to enhance autism spectrum disorder management and prediction, healthcare professionals should collaborate extensively with hospital data scientists to strengthen predictions. Ensemble methods should be used to improve final algorithms. These algorithms improve the results of autism spectrum disorder prediction in routine prenatal care of the fetus.

## Limitations and Suggestions for Further Study

Future studies should incorporate both maternal and paternal features to see whether additional pertinent information can be acquired as this study solely used maternal factors. Secondly, because of the size of the data used, in communities whose disease incidence is lower, there are signs of a greater incidence and findings that might not be useful. Future research should therefore incorporate these ideas since studies with a larger population and more attributes may open new perspectives of knowledge and help to solve the problem of ASD prediction. Future research can utilize more longitudinal survey data samples for that purpose. Adopting deep learning models and other hyperparameter tunings will allow this work to be expanded. Additional social demographic data must be considered as this was not extensively worked on in this research. And finally, the development of a smartphone or mobile application to assist both medical professionals and patients in early ASD detection.

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## Conflicts of Interest

The authors declare no conflict of interest, financial or otherwise.



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